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## Efficient protein engineering by combining computational design and directed evolution

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# Stellingen

Behorende bij het proefschrift

## **Efficient protein engineering by combining computational design and directed evolution**

Robert Floor

1. Protein thermostability should be assessed under conditions that do not allow refolding.
2. As long as homology models cannot be used to predict effective stabilizing mutations, such models should be considered inaccurate.
3. Chromatographic product analysis is the most time-efficient method to screen a library of enzyme variants.
4. Data reported by Zheng and Reetz (2010) would imply that the catalytic rate of limonene epoxide hydrolase is diffusion controlled and cannot be improved by mutations, neither of which is the case.  
*Zheng and Reetz (2010) J. Am. Chem. Soc. 132, 15744-51*
5. Praising a single characteristic of an enzyme (e.g. high stability, favorable substrate spectrum, good selectivity or ease of production) poses the risk of forgetting that an enzyme needs all these properties to be a practical catalyst.
6. Large protein tags should be avoided in biochemical experiments.
7. Creativity and ingenuity should not be replaced by market demand as main criterion for research funding.
8. The recent flood of cheap oil should not be allowed to drown the development of biobased products.
9. The use of halogenated sugars as sweeteners in food results in short-term gain and long-term environmental pain.
10. Election statements made by political parties should be falsifiable.
11. Since driving a car is the most dangerous activity in our daily life, yearly rehearsals after obtaining the driver's license should be obligatory.